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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/853,257

DATE: 05/31/2001
TIME: 15:49:32Input Set : A:\PUNIV002A.TXT
Output Set: C:\CRF3\05312001\I853257.raw

4 <110> APPLICANT: Bonnie L. Bassler
5 Brendan N. Lilley
7 <120> TITLE OF INVENTION: LUXO-SIGMA54 INTERACTIONS AND METHODS OF
8 USE

10 <130> FILE REFERENCE: PUNIV.002A

C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/853,257

C--> 12 <141> CURRENT FILING DATE: 2001-05-10

12 <150> PRIOR APPLICATION NUMBER: 60/202,999

13 <151> PRIOR FILING DATE: 2000-05-10

15 <160> NUMBER OF SEQ ID NOS: 9

17 <170> SOFTWARE: FastSEQ for Windows Version 4.0

19 <210> SEQ ID NO: 1

20 <211> LENGTH: 4003

21 <212> TYPE: DNA

22 <213> ORGANISM: Vibrio harveyi

24 <400> SEQUENCE: 1

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26 ggtatggcac tatcaggttg tgaacgccgc cgtgtagaaa ttgctcgtgc attggcagca 120
27 aacccctcagt tcattttgtt ggatgaaccg ttccgcggtg ttgacccaat ttcggttaac 180
28 gacatcaaaa aaatcatcga acacttgcgc gatcgcgcc ttggcgtgtt aatcacagac 240
29 cataacgtac gcgaacacct ggacgtttgt gaaaaagcct atatcgtaag ccaaggacac 300
30 ctcatcgcat cgggaacctc ggatgaagtt ctcaataacg agcaagtga acaagtttat 360
31 ctcggcgaac aattccgtct atgattacat taggaacggt aagattctga gcattacaag 420
32 gtaagtaaca ctgaatgaaa ccttcattac aactcaagct aggtcaacag ttagccatga 480
33 cgccacagct gcagcaagcg attcgtttgt tgcaattgtc gacgctcgat cttcaacaag 540
34 aaatccaaga agcgtttggc tccaaccgcg tactggaagt tgaagaaggc cacgatgagc 600
35 ctcaagcaaa tggatgaagc aaatcagcgt ctgaatctgc tgataaaagt gcgaacgaag 660
36 ctaacgatgc ctcaagaacc gaccttccag atagctcaga cgtgattgaa aaatctgaaa 720
37 tcagctctga gctagaaatt gataccactt gggatgacgt atatagcgca aacacgggca 780
38 gcacagcgct agcgttggt gatgacatgc ccgtctacca aggtgagacc actgaatctt 840
39 tgcattgatta ctttatgttg cagtttagct taacgccttt cagtgaacc gaccgcacca 900
40 tgcgcctcgc gattatcgat ggggtcgacg actacggcta ctttaacctc tccctgaag 960
41 aaattcacga gaccttcgac aacgaagaag tggaaattga tgaagtgaag gcggtacgta 1020
42 agcgtattca gcaatttgac ccgctcggtg tagcctctcg caatctgcaa gaatgcctac 1080
43 tgctacaact ggcaactttc cctgaagaca cgcggtggct tgctgaggcg aaaatggtgt 1140
44 tgagcgatca catcgaccac cttggcaatc gtgactacaa gctggtcatc aaagaggcta 1200
45 agcttaaaaga agcggacttg cgtgaagtat tgaagttgat tcaacaactt gaccacgctc 1260
46 caggttagtgc tatcacaccc gatgacactg aatacgtcat tccggatgtg tccgtattta 1320
47 agatcatggt taagtggaac gtctccataa accctgacag cattccgaaa ctaaaagtaa 1380
48 atcaacaata tggcgaacta ggcgaaggca acagtgaggc tagccagtaa attcgacda 1440
49 atttgcaaga ggcgaatgg ctgattaaga gcttagaaag cagaaacgag acgcttttca 1500
50 aagttgcaag atgtattgt gaacatcaac aagatttctt cgagtatggt gaagaagcca 1560
51 tgaacccaat ggtgctaaac gacgtagcat tggatgtgga catgcatgaa tgcacaattt 1620
52 ctggtgtaac aacacagaag tttatgcata cccacgctgg cattttttaa ttgaaglaet 1680
53 tcttctctag ccattgttagt acagacaatg glggagagtg ttctccaca gcaattcgcg 1740
54 cactcatcaa aaagttggtc gcagcggaga ataccgctaa gccactgagt gatagcaaaa 1800
55 ttgctgctct tctggtgac caggggattc aagtcgcgag acggacgata gcaaaatata 1860

ENTERED

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```

56 gtgaatcctt ggggtattgcc ccttcgagtc agcgtaaacg cctacttttag gcaccaattg 1920
57 aaaaggaaaag tctatgcaaa tcaatattca aggccatcac gttgatctta ccgattcaat 1980
58 gcaagaatat gttgactcta agtttcaaaa gctcgagcgg ttcttcgacc acatcaatca 2040
59 agtccatgtc gtattaaaag ttgaaaaact taaccaataa gccgaageta cgtccacat 2100
60 caatcaagga gaaatccacg cgtcatcgaa cgaagaaagt atgtatgcag caattgattc 2160
61 gctgggtgat aaattagttc gtcaacttaa caagcacaaa gaaaaactaa acagtcatta 2220
62 atcatgcaat tgagcgaaat actgtcactg gactgcacca aaagtgcggt ccattgtaca 2280
63 agtaagaaaac gtgccctcga aatgatcaga caaattgtcg ctgaaaacac gggccaagat 2340
64 tctacagaac tgtttgagtg tatgctcagc agagaaaaaa tgggtagtac tggtatcggc 2400
65 aaoggtattg ctatccctca cgttaagatg caatcaagcg acaagccat ccgagtgtta 2460
66 ctacagtgtg aagaagcaat tgaatttgac gctatcgaca acgacccgt ccacctctt 2520
67 tttgctctcc ttgtacctga agaacagtgc aaagagcacc tcaaaaacac atctctatg 2580
68 gcagagcgtc taagtgcaca gcaagtgttt aaaagcttac gtaacgctca gagcgatgaa 2640
69 gagctctacg acattatgat tcataagtaa tcaggacgat caccatgoga ttaatcgttg 2700
70 ttagcgggca ctctggtgac gggaaaaagt ttgcctcgcg cgtacttgag gacttaggtt 2760
71 actactggt agacaaccla ccggtaaaact taactgacgc gtttgttcag tcagtctctg 2820
72 agagcaaaac aaatgtcgca gtaagcatcg atattcgaaa tatccctaag aagctcaaac 2880
73 aactgaatac caogctagag aagctaaaag ctgaactgga tgtgacagta ctgtttctag 2940
74 acgogaataa ayaaacgctt ctaccccgct acagcgaaac acgtcggatt catccgctat 3000
75 caattgacag tcaatcatta tcaacttgatc aggcgattga gcttgaacaa gagatcttaa 3060
76 tgcctctgaa agcacacgca gacttagttc tgaacagtag cgtcaatct ctgcctgac 3120
77 tcagtgaacg cgtacgtatg cgtgtggaag gcgagaaacg caaagactta gtcattggtg 3180
78 ttgagtgttt tggtttcaaa taoggtttac catcagatgc cgattacgtg tttgatgtgc 3240
79 gtttcttgcc aaacccacac tgggagccag cactggccgc tctcactggt ttagatggcc 3300
80 cgatcggcgc ctctcttagag caacaccagt cggtaactga tctgaaatac caaattgaaa 3360
81 gctttattga gacttggtta ccactattag agaaaaacaa ccgtagttac ctgaacgtg 3420
82 cgattggttg tactggtggt aaacacccgt cgggttatct tactcaaaaa attggtgagt 3480
83 tctttcgga caaaggacac caagtacaaa ttgcacacac ttcattggaa aagaacgtta 3540
84 aggaataacg gtggaattaa gtogtaaagt actgatccaa aaccgactag gcttgcacgc 3600
85 tctgctggca gttaaaactg tagaactagc acaaagcttc gacgcggtga ttaccatoga 3660
86 caacgaagaa gacaaaaccc cgacccgaga cagcgtcatg ggattgctga tgcctggaac 3720
87 agcccaagga caatacgtga ccacccacgc cactggcgat caatctgagc aagctcttga 3780
88 tgcggtctgc catttgatcg aagataagtt tgacgaagcg gagtgattca ctgcctttt 3840
89 tattatctct agccagatat cccacataag tttaacctcc tgcctaaaatt ccgacaaaata 3900
90 attttgtoga ctctcataag ttgttattaa aagtgcccta gaattaaagt attattcaaa 3960
91 gcattgtaaa taccaggaat tgggaggaat gaatggcaga gca 4003

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92 <210> SEQ ID NO: 2

93 <211> LENGTH: 491

94 <212> TYPE: PRT

95 <213> ORGANISM: Vibrio harveyi

96 <400> SEQUENCE: 2

97 Met Lys Pro Ser Leu Gln Leu Lys Leu Gly Gln Gln Leu Ala Met Thr

100 1 5 10 15

101 Pro Gln Leu Gln Gln Ala Ile Arg Leu Leu Gln Leu Ser Thr Leu Asp

102 20 25 30

103 Leu Gln Gln Glu Ile Gln Glu Ala Leu Asp Ser Asn Pro Leu Leu Glu

104 35 40 45

105 Val Glu Glu Gly His Asp Glu Pro Gln Ala Asn Gly Glu Asp Lys Ser

106 50 55 60

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107 Ala Ser Glu Ser Ala Asp Lys Ser Ala Asn Glu Ala Asn Asp Ala Ser
108 65 70 75 80
109 Glu Pro Asp Leu Pro Asp Ser Ser Asp Val Ile Glu Lys Ser Glu Ile
110 85 90 95
111 Ser Ser Glu Leu Glu Ile Asp Thr Thr Trp Asp Asp Val Tyr Ser Ala
112 100 105 110
113 Asn Thr Gly Ser Thr Gly Leu Ala Leu Asp Asp Asp Met Pro Val Tyr
114 115 120 125
115 Gln Gly Glu Thr Thr Glu Ser Leu His Asp Tyr Leu Met Trp Gln Leu
116 130 135 140
117 Asp Leu Thr Pro Phe Ser Glu Thr Asp Arg Thr Ile Ala Leu Ala Ile
118 145 150 155 160
119 Ile Asp Ala Val Asp Asp Tyr Gly Tyr Leu Thr Leu Ser Pro Glu Glu
120 165 170 175
121 Ile His Glu Ser Phe Asp Asn Glu Glu Val Glu Leu Asp Glu Val Glu
122 180 185 190
123 Ala Val Arg Lys Arg Ile Gln Gln Phe Asp Pro Leu Gly Val Ala Ser
124 195 200 205
125 Arg Asn Leu Gln Glu Cys Leu Leu Leu Gln Leu Ala Thr Phe Pro Glu
126 210 215 220
127 Asp Thr Pro Trp Leu Ala Glu Ala Lys Met Val Leu Ser Asp His Ile
128 225 230 235 240
129 Asp His Leu Gly Asn Arg Asp Tyr Lys Leu Val Ile Lys Glu Ala Lys
130 245 250 255
131 Leu Lys Glu Ala Asp Leu Arg Glu Val Leu Lys Leu Ile Gln Gln Leu
132 260 265 270
133 Asp Pro Arg Pro Gly Ser Arg Ile Thr Pro Asp Asp Thr Glu Tyr Val
134 275 280 285
135 Ile Pro Asp Val Ser Val Phe Lys Asp His Gly Lys Trp Thr Val Ser
136 290 295 300
137 Ile Asn Pro Asp Ser Ile Pro Lys Leu Lys Val Asn Gln Gln Tyr Ala
138 305 310 315 320
139 Gln Leu Gly Lys Gly Asn Ser Ala Asp Ser Gln Tyr Ile Arg Ser Asn
140 325 330 335
141 Leu Gln Glu Ala Lys Trp Leu Ile Lys Ser Leu Glu Ser Arg Asn Glu
142 340 345 350
143 Thr Leu Leu Lys Val Ala Arg Cys Ile Val Glu His Gln Gln Asp Phe
144 355 360 365
145 Phe Glu Tyr Gly Glu Glu Ala Met Lys Pro Met Val Leu Asn Asp Val
146 370 375 380
147 Ala Leu Asp Val Asp Met His Glu Ser Thr Ile Ser Arg Val Thr Thr
148 385 390 395 400
149 Gln Lys Ala Met His Thr Pro Arg Gly Ile Phe Glu Leu Lys Tyr Phe
150 405 410 415
151 Phe Ser Ser His Val Ser Thr Asp Asn Gly Gly Glu Cys Ser Ser Ile
152 420 425 430
153 Ala Ile Arg Ala Leu Ile Lys Lys Leu Val Ala Ala Glu Asn Thr Ala
154 435 440 445
155 Lys Pro Leu Ser Asp Ser Lys Ile Ala Ala Leu Leu Ala Asp Gln Gly

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```

156      450      455      460
157 Ile Gln Val Ala Arg Arg Thr Ile Ala Lys Tyr Arg Glu Ser Leu Gly
158 465      470      475      480
159 Ile Ala Pro Ser Ser Gln Arg Lys Arg Leu Leu
160      485      490
163 <210> SEQ ID NO: 3
164 <211> LENGTH: 476
165 <212> TYPE: DNA
166 <213> ORGANISM: Vibrio harveyi
167 <400> SEQUENCE: 3
168 atgaaacatt cattaact caagctaggt caacagttag caatgaacgc acagctgcag 60
169 caagcgatgc ctatgttgca attgtcgacg ctcgatcttc aacaagaaat caagaagcg 120
170 ttggactcca acccgctact ggaagtggaa gaaggccacg atgagcctca agcaaatggt 180
171 gaagacaaat cagcgtctga atctgctgat aaaagtgcga acgaagctaa cgatgcctca 240
172 gaacccgacc ttccagatag ctcaagcgtg attgaaaaat ctgaaatcag ctctgagcta 300
173 gaaattgata ccacttggga tgacgtatat agcgcaaaca cgggcagcac aggcctagcg 360
174 cgggatgatg acatgcccggt ctaccaaggt gagaccactg aatctttgca tgattacctt 420
175 atgttgcagt tagacttaac gcccttcagt gaaaccgacc gcaccatgcg cctcgc 476
176 <210> SEQ ID NO: 4
177 <211> LENGTH: 6
178 <212> TYPE: PRT
179 <213> ORGANISM: Artificial Sequence
180 <220> FEATURE:
181 <223> OTHER INFORMATION: portion of consensus sequence of sigma-54 domains
182 <221> NAME/KEY: VARIANT
183 <222> LOCATION: (1)...(6)
184 <223> OTHER INFORMATION: Xaa = Trp or Phe
185 <400> SEQUENCE: 4
W--> 191 Xaa Phe Pro Gly Asn Val
192 1 5
193 <210> SEQ ID NO: 5
194 <211> LENGTH: 6
195 <212> TYPE: PRT
196 <213> ORGANISM: Artificial Sequence
197 <220> FEATURE:
198 <223> OTHER INFORMATION: portion of consensus sequence of sigma-54 domains
199 <221> NAME/KEY: VARIANT
200 <222> LOCATION: (1)...(6)
201 <223> OTHER INFORMATION: Xaa = Val, Ala, Asp, Glu, Gly
202 <400> SEQUENCE: 5
W--> 208 Glu Leu Phe Gly His Xaa
209 1 5
210 <210> SEQ ID NO: 6
211 <211> LENGTH: 2
212 <212> TYPE: DNA
213 <213> ORGANISM: Artificial Sequence
214 <220> FEATURE:
215 <223> OTHER INFORMATION: upstream primer to amplify rpoN gene
216 <400> SEQUENCE: 6

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20
221 ggycaacart tagcsatgac
223 <210> SEQ ID NO: 7
224 <211> LENGTH: 21
225 <212> TYPE: DNA
226 <213> ORGANISM: Artificial Sequence
228 <220> FEATURE:
229 <223> OTHER INFORMATION: downstream primer to amplify rpoN gene
231 <400> SEQUENCE: 7 21
232 catggytctc tcccatatc c
234 <210> SEQ ID NO: 8
235 <211> LENGTH: 25
236 <212> TYPE: DNA
237 <213> ORGANISM: Artificial Sequence
239 <220> FEATURE:
240 <223> OTHER INFORMATION: upstream primer used to amplify rpoN gene
242 <400> SEQUENCE: 8 25
243 ggaacggtag aattctgagc attac
245 <210> SEQ ID NO: 9
246 <211> LENGTH: 28
247 <212> TYPE: DNA
248 <213> ORGANISM: Artificial Sequence
250 <220> FEATURE:
251 <223> OTHER INFORMATION: downstream primer used to amplify rpoN gene
253 <400> SEQUENCE: 9 28
254 ccttttgaat tcgtgcctaa agtaggcg

VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:191 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4

L:208 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5